

PCT09

RAW SEQUENCE LISTING

DATE: 11/12/2001

PATENT APPLICATION: US/09/744,910B

TIME: 18:28:54

Input Set : A:\Asahi2pc.app

Output Set: N:\CRF3\11122001\I744910B.raw

3 <110> APPLICANT: MATSUYAMA, KENJI
 4 SHIRAI, TAKASHI
 5 ETOH, TAKASHI
 7 <120> TITLE OF INVENTION: ANTIBODIES FOR DETECTING MICROORGANISMS
 9 <130> FILE REFERENCE: ASAHI-2-PC-1
 11 <140> CURRENT APPLICATION NUMBER: 09/744,910B
 12 <141> CURRENT FILING DATE: 2001-05-17
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04122
 15 <151> PRIOR FILING DATE: 1999-07-30
 17 <150> PRIOR APPLICATION NUMBER: JP 10/230204
 18 <151> PRIOR FILING DATE: 1998-07-31
 20 <160> NUMBER OF SEQ ID NOS: 22
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 369
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Haemophilus influenzae
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(369)
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 35 Met Ser Leu Thr Asn Glu Gln Ile Ile Glu Ala Ile Ala Ser Lys Thr
 36 1 5 10 15
 38 gta act gaa atc gtt gaa tta atc gca gcg atg gaa gaa aaa ttc ggt 96
 39 Val Thr Glu Ile Val Glu Leu Ile Ala Ala Met Glu Glu Lys Phe Gly
 40 20 25 30
 42 gtt tca gca gcg gca gca gta gca gca gct cca gca gca ggc ggt gca 144
 43 Val Ser Ala Ala Ala Ala Val Ala Ala Ala Pro Ala Ala Gly Gly Ala
 44 35 40 45
 46 gcg gca gca gaa gaa aaa act gaa ttc gac gtt gta ctt aaa tct gca 192
 47 Ala Ala Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Lys Ser Ala
 48 50 55 60
 50 ggt gcg aac aaa gta gca gta att aaa gca gta cgt ggt gca act ggt 240
 51 Gly Ala Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly
 52 65 70 75 80
 54 tta ggc tta aaa gaa gct aaa gat tta gtt gaa tct gct cca gct aac 288
 55 Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Asn
 56 85 90 95
 58 tta aaa gaa ggc gtt tct aaa gaa gaa gct gaa gca ctt aag aaa gaa 336
 59 Leu Lys Glu Gly Val Ser Lys Glu Glu Ala Glu Ala Leu Lys Lys Glu
 60 100 105 110
 62 tta gaa gaa gcg ggt gca gaa gta gaa gtt aaa 369
 63 Leu Glu Glu Ala Gly Ala Glu Val Glu Val Lys
 64 115 120
 67 <210> SEQ ID NO: 2
 68 <211> LENGTH: 123

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69 <212> TYPE: PRT
70 <213> ORGANISM: Haemophilus influenzae
72 <400> SEQUENCE: 2
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74   1           5           10           15
76 Val Thr Glu Ile Val Glu Leu Ile Ala Ala Met Glu Glu Lys Phe Gly
77           20           25           30
79 Val Ser Ala Ala Ala Ala Val Ala Ala Ala Pro Ala Ala Gly Gly Ala
80   35           40           45
82 Ala Ala Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Lys Ser Ala
83   50           55           60
85 Gly Ala Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly
86   65           70           75           80
88 Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Asn
89           85           90           95
91 Leu Lys Glu Gly Val Ser Lys Glu Glu Ala Glu Ala Leu Lys Lys Glu
92           100          105          110
94 Leu Glu Glu Ala Gly Ala Glu Val Glu Val Lys
95           115          120
98 <210> SEQ ID NO: 3
99 <211> LENGTH: 375
100 <212> TYPE: DNA
101 <213> ORGANISM: Helicobacter pylori
103 <220> FEATURE:
104 <221> NAME/KEY: CDS
105 <222> LOCATION: (1)..(375)
107 <400> SEQUENCE: 3
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109 Met Ala Ile Ser Lys Glu Glu Val Leu Glu Tyr Ile Gly Ser Leu Ser
110   1           5           10           15
112 gtt tta gag ctt tct gaa ttg gtt aaa atg ttt gag gaa aaa ttt ggc   96
113 Val Leu Glu Leu Ser Glu Leu Val Lys Met Phe Glu Glu Lys Phe Gly
114           20           25           30
116 gtg agc gcg act cca acg gtc gta gcg ggt gcg gct gta gct ggc ggt   144
117 Val Ser Ala Thr Pro Thr Val Val Ala Gly Ala Ala Val Ala Gly Gly
118           35           40           45
120 gca gcg gct gag agc gaa gaa aaa acc gaa ttt aat gtg att ttg gcc   192
121 Ala Ala Ala Glu Ser Glu Glu Lys Thr Glu Phe Asn Val Ile Leu Ala
122           50           55           60
124 gat agc ggt gct gaa aaa att aag gtg att aaa gtg gtt cgt gaa atc   240
125 Asp Ser Gly Ala Glu Lys Ile Lys Val Ile Lys Val Val Arg Glu Ile
126   65           70           75           80
128 act gga ctt ggc ctg aaa gaa gct aaa gac gct acc gaa aaa acc cct   288
129 Thr Gly Leu Gly Leu Lys Glu Ala Lys Asp Ala Thr Glu Lys Thr Pro
130           85           90           95
132 cat gtg ctt aaa gag ggc gtg aat aaa gaa gaa gct gaa acc atc aag   336
133 His Val Leu Lys Glu Gly Val Asn Lys Glu Glu Ala Glu Thr Ile Lys
134           100          105          110
136 aag aaa ctt gaa gaa gta ggc gct aag gtt gaa gtc aag   375

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137 Lys Lys Leu Glu Glu Val Gly Ala Lys Val Glu Val Lys
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142 <211> LENGTH: 125
143 <212> TYPE: PRT
144 <213> ORGANISM: Helicobacter pylori
146 <400> SEQUENCE: 4
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150 Val Leu Glu Leu Ser Glu Leu Val Lys Met Phe Glu Glu Lys Phe Gly
151      20          25          30
153 Val Ser Ala Thr Pro Thr Val Val Ala Gly Ala Ala Val Ala Gly Gly
154      35          40          45
156 Ala Ala Ala Glu Ser Glu Glu Lys Thr Glu Phe Asn Val Ile Leu Ala
157      50          55          60
159 Asp Ser Gly Ala Glu Lys Ile Lys Val Ile Lys Val Val Arg Glu Ile
160      65          70          75          80
162 Thr Gly Leu Gly Leu Lys Glu Ala Lys Asp Ala Thr Glu Lys Thr Pro
163      85          90          95
165 His Val Leu Lys Glu Gly Val Asn Lys Glu Glu Ala Glu Thr Ile Lys
166      100         105         110
168 Lys Lys Leu Glu Glu Val Gly Ala Lys Val Glu Val Lys
169      115          120          125
172 <210> SEQ ID NO: 5
173 <211> LENGTH: 366
174 <212> TYPE: DNA
175 <213> ORGANISM: Streptococcus pneumoniae
177 <220> FEATURE:
178 <221> NAME/KEY: CDS
179 <222> LOCATION: (1)..(366)
181 <400> SEQUENCE: 5
182 atg gca ttg aac att gaa aac att att gct gaa att aaa gaa gct tca 48
183 Met Ala Leu Asn Ile Glu Asn Ile Ile Ala Glu Ile Lys Glu Ala Ser
184   1          5          10          15
186 atc ctt gaa ttg aac gac ctt gta aaa gct atc gaa gaa gaa ttt ggt 96
187 Ile Leu Glu Leu Asn Asp Leu Val Lys Ala Ile Glu Glu Glu Phe Gly
188      20          25          30
190 gta act gca gct gct cct gta gct gtt gct gca gct gat gca gct gat 144
191 Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Asp Ala Ala Asp
192      35          40          45
194 gct ggt gct gct aaa gat tca ttc gac gtt gaa ttg aca tct gca ggc 192
195 Ala Gly Ala Ala Lys Asp Ser Phe Asp Val Glu Leu Thr Ser Ala Gly
196      50          55          60
198 gac aaa aaa gtt ggc gtt atc aaa gtt gta cgt gaa atc act ggt ctt 240
199 Asp Lys Lys Val Gly Val Ile Lys Val Val Arg Glu Ile Thr Gly Leu
200      65          70          75          80
202 ggt ctt aaa gaa gct aaa gaa ctt gtt gac ggt gca cca gca ctt gtt 288
203 Gly Leu Lys Glu Ala Lys Glu Leu Val Asp Gly Ala Pro Ala Leu Val
204      85          90          95

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206 aaa gaa ggc gtt gca act gca gaa gct gaa gaa atc aaa gct aaa ttg      336
207 Lys Glu Gly Val Ala Thr Ala Glu Ala Glu Glu Ile Lys Ala Lys Leu
208          100                      105                      110
210 gaa gaa gct gga gct tca gtt act ctt aaa                                366
211 Glu Glu Ala Gly Ala Ser Val Thr Leu Lys
212          115                      120
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 122
217 <212> TYPE: PRT
218 <213> ORGANISM: Streptococcus pneumoniae
220 <400> SEQUENCE: 6
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222   1          5          10          15
224 Ile Leu Glu Leu Asn Asp Leu Val Lys Ala Ile Glu Glu Glu Phe Gly
225          20          25          30
227 Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Ala Asp Ala Ala Asp
228          35          40          45
230 Ala Gly Ala Ala Lys Asp Ser Phe Asp Val Glu Leu Thr Ser Ala Gly
231          50          55          60
233 Asp Lys Lys Val Gly Val Ile Lys Val Val Arg Glu Ile Thr Gly Leu
234   65          70          75          80
236 Gly Leu Lys Glu Ala Lys Glu Leu Val Asp Gly Ala Pro Ala Leu Val
237          85          90          95
239 Lys Glu Gly Val Ala Thr Ala Glu Ala Glu Glu Ile Lys Ala Lys Leu
240          100          105          110
242 Glu Glu Ala Gly Ala Ser Val Thr Leu Lys
243          115          120
246 <210> SEQ ID NO: 7
247 <211> LENGTH: 369
248 <212> TYPE: DNA
249 <213> ORGANISM: Neisseria gonorrhoeae
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (1)..(369)
255 <400> SEQUENCE: 7
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258   1          5          10          15
260 gta atg gaa ttg aat gac ctg gtt aaa gct ttt gaa gaa aaa ttc ggt      96
261 Val Met Glu Leu Asn Asp Leu Val Lys Ala Phe Glu Glu Lys Phe Gly
262          20          25          30
264 gtt tct gct gct gct gtt gca gtt gca ggt cct gct ggt gcc ggt gct      144
265 Val Ser Ala Ala Ala Val Ala Val Ala Gly Pro Ala Gly Ala Gly Ala
266          35          40          45
268 gcc gat gct gaa gaa aaa acc gaa ttt gat gtc gtt ttg gct tct gcc      192
269 Ala Asp Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Ala Ser Ala
270          50          55          60
272 ggc gat caa aaa gtc ggc gtg att aaa gtt gtc cgt gca att act ggt      240
273 Gly Asp Gln Lys Val Gly Val Ile Lys Val Val Arg Ala Ile Thr Gly

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274 65          70          75          80
276 ttg ggt ctg aaa gaa gct aaa gac atc gtt gac ggc gca cct aaa acc 288
277 Leu Gly Leu Lys Glu Ala Lys Asp Ile Val Asp Gly Ala Pro Lys Thr
278          85          90          95
280 att aaa gag ggt gtt tct aaa gct gaa gcc gaa gac atc caa aaa caa 336
281 Ile Lys Glu Gly Val Ser Lys Ala Glu Ala Glu Asp Ile Gln Lys Gln
282          100          105          110
284 ctg gaa gca gca ggc gct aaa gtc gaa atc aaa 369
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286          115          120
289 <210> SEQ ID NO: 8
290 <211> LENGTH: 123
291 <212> TYPE: PRT
292 <213> ORGANISM: Neisseria gonorrhoeae
294 <400> SEQUENCE: 8
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299          20          25          30
301 Val Ser Ala Ala Ala Val Ala Val Ala Gly Pro Ala Gly Ala Gly Ala
302          35          40          45
304 Ala Asp Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Ala Ser Ala
305          50          55          60
307 Gly Asp Gln Lys Val Gly Val Ile Lys Val Val Arg Ala Ile Thr Gly
308 65          70          75          80
310 Leu Gly Leu Lys Glu Ala Lys Asp Ile Val Asp Gly Ala Pro Lys Thr
311          85          90          95
313 Ile Lys Glu Gly Val Ser Lys Ala Glu Ala Glu Asp Ile Gln Lys Gln
314          100          105          110
316 Leu Glu Ala Ala Gly Ala Lys Val Glu Ile Lys
317          115          120
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 369
322 <212> TYPE: DNA
323 <213> ORGANISM: Neisseria meningitidis
325 <220> FEATURE:
326 <221> NAME/KEY: CDS
327 <222> LOCATION: (1)..(369)
329 <400> SEQUENCE: 9
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331 Met Ala Ile Thr Lys Glu Asp Ile Leu Glu Ala Val Gly Ser Leu Thr
332 1          5          10          15
334 gta atg gaa ttg aac gac ttg gtt aaa gct ttt gaa gaa aaa ttc ggt 96
335 Val Met Glu Leu Asn Asp Leu Val Lys Ala Phe Glu Glu Lys Phe Gly
336          20          25          30
338 gtt tct gct gct gct gtt gca gtt gca ggt cct gct ggt gcc ggt gct 144
339 Val Ser Ala Ala Ala Val Ala Val Ala Gly Pro Ala Gly Ala Gly Ala
340          35          40          45
342 gcc gat gct gaa gaa aaa acc gaa ttt gat gtc gtt ttg gct tct gcc 192

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